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SEQUENCE LISTING

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PHARMALOGICALS RESEARCH PTE., LTD.

<120> ANTIBODIES AGAINST LESIONAL TISSUES

<130> C1-A0230P

<140> JP 2002-339241

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<160> 188

<170> PatentIn version 3.1

<210> 1

<211> 360

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(360)

<223>

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

tca gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc 96
Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe

2 / 1 4 1

20

25

30

tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

gga tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt 192
Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe

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60

cag gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac 240
Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
65 70 75 80

atg gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt 288
Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa 336
Ala Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln
100 105 110

ggg cca atg gtc acc gtc tct tca 360
Gly Pro Met Val Thr Val Ser Ser
115 120

<210> 2

<211> 120

<212> PRT

<213> Homo sapiens

<400> 2

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

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3 / 1 4 1

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
50 55 60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
65 70 75 80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln
100 105 110

Gly Pro Met Val Thr Val Ser Ser
115 120

<210> 3

<211> 366

<212> DNA

<213> Homo sapiens

<220>

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<222> (1)..(366)

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<400> 3

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Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
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4 / 1 4 1

tcc	ctg	aga	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	acc	ttc	agt	agc	aat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Asn	
20															30	
ggc	atg	cac	tgg	gtc	cgc	cag	gct	cca	ggc	aag	ggg	ctg	gag	tgg	gtg	144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
35															45	
gca	gtt	ata	tgg	tat	gat	gga	agt	aat	aaa	tac	tat	gca	gac	tcc	gtg	192
Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	
50															60	
aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	aat	tcc	aag	aac	aca	ctg	tat	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
65															80	
ctg	caa	atg	aac	agc	ctg	aga	gcc	gag	gac	acg	gct	gtg	tat	tac	tgt	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
85															95	
gcg	aga	gat	cac	ggc	ctt	ggt	gat	caa	gcc	tcc	tgg	ttc	gac	ccc	tgg	336
Ala	Arg	Asp	His	Gly	Leu	Gly	Asp	Gln	Ala	Ser	Trp	Phe	Asp	Pro	Trp	
100															110	
ggc	cag	gga	acc	ctg	gtc	acc	gtc	tcc	tca							366
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
115															120	

<210> 4

<211> 122

<212> PRT

<213> Homo sapiens

<400> 4

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Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 5

<211> 366

<212> DNA

<213> Homo sapiens

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<222> (1)..(366)

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1 5 10 15	
tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc aat	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn	
20 25 30	
ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg	144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
gca gtt ata tgg tat gat gga agt aat aaa tac tat gca gac tcc gtg	192
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val	
50 55 60	
aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac aca ctg tat	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gcg aga gat cac ggc ctt ggt gat caa gcc tcc tgg ttc gac ccc tgg	336
Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp	
100 105 110	
ggc cag gga acc ctg gtc acc gtc tcc tca	366
Gly Gln Gly Thr Leu Val Thr Val Ser Ser	
115 120	

<210> 6

<211> 122

<212> PRT

7 / 1 4 1

<213> Homo sapiens

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Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 7

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<212> DNA

<213> Homo sapiens

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8 / 1 4 1

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1 5 10 15

aca gtg aca atc tcc tgc aag gtt tct gga cac aac ttc atc gac cac 96
Thr Val Thr Ile Ser Cys Lys Val Ser Gly His Asn Phe Ile Asp His
20 25 30

tac atg cat tgg gta caa cag gcc cct gga aaa ggg ctt gac tgg atg 144
Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Asp Trp Met
35 40 45

gga cta att gac cct gaa gat ggt cag acg aaa tat tca gag agg ttt 192
Gly Leu Ile Asp Pro Glu Asp Gly Gln Thr Lys Tyr Ser Glu Arg Phe
50 55 60

gag ggc aga gtc aca att acc gcg gac aag tca aca gac aca acc tac 240
Glu Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asp Thr Thr Tyr
65 70 75 80

ttg gag gtg agc ggc ctg aga tcg gaa gac acg gcc gtt tat ttc tgt 288
Leu Glu Val Ser Gly Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

aca acg gac ttg ggt gac ttg aat tat tgg aac cct ggt cac cgt ctc 336
Thr Thr Asp Leu Gly Asp Leu Asn Tyr Trp Asn Pro Gly His Arg Leu
100 105 110

ctc a 340
Leu

9 / 1 4 1

<210> 8
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<213> Homo sapiens

<400> 8

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Thr
1 5 10 15

Thr Val Thr Ile Ser Cys Lys Val Ser Gly His Asn Phe Ile Asp His
20 25 30

Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Asp Trp Met
35 40 45

Gly Leu Ile Asp Pro Glu Asp Gly Gln Thr Lys Tyr Ser Glu Arg Phe
50 55 60

Glu Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asp Thr Thr Tyr
65 70 75 80

Leu Glu Val Ser Gly Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Thr Thr Asp Leu Gly Asp Leu Asn Tyr Trp Asn Pro Gly His Arg Leu
100 105 110

Leu

<210> 9
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1 0 / 1 4 1

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<222> (1).. (366)

<223>

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Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc aat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gca gtt ata tgg tat gat gga agt aat aaa tac tat gca gac tcc gtg 192
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac aca ctg tat 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg aga gat cac ggc ctt ggt gat caa gcc tcc tgg ttc gac ccc tgg 336
Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp
100 105 110

ggc cag gga acc ctg gtc acc gtc tcc tca 366
Gly Gln Gly Thr Leu Val Thr Val Ser Ser

1 1 / 1 4 1

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<210> 10

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<212> PRT

<213> Homo sapiens

<400> 10

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 11

<211> 381

1 2 / 1 4 1

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<213> Homo sapiens

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<222> (1)..(381)

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tct ctg aag atc tcc tgt cag ggt tct gga tac aca ttt agc aat tac 96
Ser Leu Lys Ile Ser Cys Gln Gly Ser Gly Tyr Thr Phe Ser Asn Tyr
20 25 30

tgg atc gcc tgg gtg cgc cag agg ccc ggg aaa ggc ctg gag tgg atg 144
Trp Ile Ala Trp Val Arg Gln Arg Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

ggg atc atc tat cct ggt gac tct gat atc aaa tac agt ccg tcc ttc 192
Gly Ile Ile Tyr Pro Gly Asp Ser Asp Ile Lys Tyr Ser Pro Ser Phe
50 55 60

caa ggc cat gtc acc atc tca gcc gac acg tcc atg aac acc gcc tac 240
Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser Met Asn Thr Ala Tyr
65 70 75 80

ctg cag tgg aac acc ctg aag gcc tcg gac acc gcc atg tac tac tgt 288
Leu Gln Trp Asn Thr Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

gcg aga cat aaa ggg acc agg ttc ggg gag gtt ttg gcg gtt ggc aac 336
Ala Arg His Lys Gly Thr Arg Phe Gly Glu Val Leu Ala Val Gly Asn
100 105 110

1 3 / 1 4 1

tgg ttc gac ccc tgg ggc cag gga acc ctg gtc acc gtc tcc tca 381
Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

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<213> Homo sapiens

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Gly Lys Lys Pro Gly Glu
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Ser Leu Lys Ile Ser Cys Gln Gly Ser Gly Tyr Thr Phe Ser Asn Tyr
20 25 30

Trp Ile Ala Trp Val Arg Gln Arg Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Ile Lys Tyr Ser Pro Ser Phe
50 55 60

Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser Met Asn Thr Ala Tyr
65 70 75 80

Leu Gln Trp Asn Thr Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg His Lys Gly Thr Arg Phe Gly Glu Val Leu Ala Val Gly Asn
100 105 110

Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

14/141

<210> 13
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1	5	10	15
tcg gtg aaa ttc tcc tgc aag gct tcc gga ggc agc ttc agc aac tat			96
Ser Val Lys Phe Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Asn Tyr			
20	25	30	
gct atc acc tgg gtg cga cag gcc cct gga caa ggt ctt gag tgg atg			144
Ala Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met			
35	40	45	
gga agg atc atc cct atc ttt ggt ata cca aac tac gca cag gaa ttc			192
Gly Arg Ile Ile Pro Ile Phe Gly Ile Pro Asn Tyr Ala Gln Glu Phe			
50	55	60	
cag ggc aga gtc acg att acc gcc gac gat tcc acg acc aca gtc tac			240
Gln Gly Arg Val Thr Ile Thr Ala Asp Asp Ser Thr Thr Val Tyr			
65	70	75	80
atg gaa ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt			288
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	

15/141

gca aga gat aat tca ata gga gca cct gat act tgg tgg ttc gac ccc 336
Ala Arg Asp Asn Ser Ile Gly Ala Pro Asp Thr Trp Trp Phe Asp Pro
100 105 110

tgg ggc cag gga cca cgg tca ccg tct cct ca 368
Trp Gly Gln Gly Pro Arg Ser Pro Ser Pro
115 120

<210> 14
<211> 122
<212> PRT
<213> Homo sapiens

<400> 14
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Leu Lys Thr Pro Gly Ser
1 5 10 15

Ser Val Lys Phe Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Asn Tyr
20 25 30

Ala Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Phe Gly Ile Pro Asn Tyr Ala Gln Glu Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Asp Ser Thr Thr Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Asn Ser Ile Gly Ala Pro Asp Thr Trp Trp Phe Asp Pro
100 105 110

16 / 141

Trp Gly Gln Gly Pro Arg Ser Pro Ser Pro

115 120

<210> 15

<211> 360

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(360)

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

tca gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc 96
Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe
20 25 30

tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

gga tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt 192
Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
50 55 60

cag gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac 240
Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
65 70 75 80

atg gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt 288

1 7 / 1 4 1

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85

90

95

gcg aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa
Ala Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln

100

105

110

336

ggg aca atg gtc acc gtc tct tca
Gly Thr Met Val Thr Val Ser Ser

115

120

360

<210> 16

<211> 120

<212> PRT

<213> Homo sapiens

<400> 16

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe

20

25

30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe

50

55

60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr

65

70

75

80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys

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18 / 141

Ala Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln

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105

110

Gly Thr Met Val Thr Val Ser Ser

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120

<210> 17

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<212> DNA

<213> Homo sapiens

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<222> (1)..(363)

<223>

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Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc aat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gca gtt ata tgg tat gat gga agt aat aaa tac tat gca gac tcc gtg 192
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac aca ctg tat 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

19 / 141

65

70

75

80

ctg caa atg aac agc ctg agg gcc gag gac acg gct gtg tat tac tgt
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

288

85

90

95

gct aga gat cac ggc ctt ggt gat caa gcc tcc tgg ttc gac ccc tgg
Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp

336

100

105

110

ggc cag gga acc ctg gtc acc gtc tcc tc
Gly Gln Gly Thr Leu Val Thr Val Ser

365

115

120

<210> 18

<211> 121

<212> PRT

<213> Homo sapiens

<400> 18

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn

20

25

30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

20 / 141

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp

100

105

110

Gly Gln Gly Thr Leu Val Thr Val Ser

115

120

<210> 19

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(366)

<223>

<400> 19

cag gtc cag ctg gcg caa tct gga gga ggc gtg gtc cag cct ggg agg
Gln Val Gln Leu Ala Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg

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10

15

48

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc agc ttc agt agc tat
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr

20

25

30

96

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

144

gca gtt ata tgg tat gat gga agc tat aaa tac tat gca gaa tcc gtg
Ala Val Ile Trp Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Glu Ser Val

50

55

60

192

21 / 141

aag ggc cga ttc atc atc tcc aga gac aat tcc aag aac acc ctg tat 240
Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtc tat tac tgt 288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg aga gat cgg ggg tcg gtg gag atg gct aca atc gcg gac tac tgg 336
Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp
100 105 110

ggc cag gga acc ctg gtc acc gtc tcc tca 366
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 20

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<212> PRT

<213> Homo sapiens

<400> 20

Gln Val Gln Leu Ala Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Glu Ser Val
50 55 60

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Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 21

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(366)

<223>

<400> 21

cag gtc cag ctg gtg caa tct ggg gga ggc gtg gtc cag cct ggg agg 48
Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc agc ttc agt agc tat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

23 / 141

gca gtt ata tgg tat gat gga agt tat aaa tac tat gca gaa tcc gtg 192
Ala Val Ile Trp Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Glu Ser Val
50 55 60

aag ggc cga ttc atc atc tcc aga gac aat tcc aag aac acc ctg tat 240
Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg aga gat cgg ggg tcg gta gag atg gct aca atc gcg gac tac tgg 336
Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp
100 105 110

ggc cag gga acc ctg gtc acc gtc tcc tca 366
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 22

<211> 122

<212> PRT

<213> Homo sapiens

<400> 22

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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Ala Val Ile Trp Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 23

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(366)

<223>

<400> 23

cag gtc cag ctg gtg caa tct ggg gga ggc gtg gtc cag cct ggg agg 48

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc agc ttc agt agc tat 96

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr

20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144

25/141

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

gca gtt ata tgg tat gat gga agt tat aaa tac tat gca gaa tcc gtg
Ala Val Ile Trp Tyr Asp Gly Ser Tyr Lys Tyr Ala Glu Ser Val

50 55 60

aag ggc cga ttc atc atc tcc aga gac aat tcc aag aac acc ctg tat
Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtc tat tac tgt
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

gcg aga gat cgg ggg tcg gta gag atg gct aca atc gcg gac tac tgg
Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp

100 105 110

ggc cag gga acc ctg gtc acc gtc tcc tca
Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

288

336

366

<210> 24

<211> 122

<212> PRT

<213> Homo sapiens

<400> 24

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr

20 25 30

2 6 / 1 4 1

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Tyr Lys Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 25

<211> 370

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (369)

<223>

<400> 25

cag gta cag ctg cag cag tca ggt cca gga ctg gtg aag ccc tcg cag 48

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

acc ctc tca ctc acc tgt gcc atc tcc ggg gac agt gtc tct agc aac 96

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn

27 / 141

20

25

30

agt gct gct tgg cac tgg atc agg cag tcc cca tcg aga ggc ctt gag 144
Ser Ala Ala Trp His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu

35

40

45

tgg ctg gga agg aca tac tac agg tcc aag tgg tat aat gat tat aca 192
Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Thr

50

55

60

gtg tct gtg aaa agt cga ata acc atc aag cca gac aca tcc aag aac 240
Val Ser Val Lys Ser Arg Ile Thr Ile Lys Pro Asp Thr Ser Lys Asn
65 70 75 80

cag ttc tcc ctg cag ctg aac tct gtg act ccc gag gac acg gct gtg 288
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

tat tac tgt gca aga tca cag gaa gag cac cgg tcg ttg gat gat gct 336
Tyr Tyr Cys Ala Arg Ser Gln Glu Glu His Arg Ser Leu Asp Asp Ala
100 105 110

ttt gat atc tgg gac cac ggt cac cgt ctc ctc a 370
Phe Asp Ile Trp Asp His Gly His Arg Leu Leu
115 120

<210> 26

<211> 123

<212> PRT

<213> Homo sapiens

<400> 26

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1

5

10

15

28/141

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
20 25 30

Ser Ala Ala Trp His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Thr
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Lys Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Ser Gln Glu Glu His Arg Ser Leu Asp Asp Ala
100 105 110

Phe Asp Ile Trp Asp His Gly His Arg Leu Leu
115 120

<210> 27

<211> 360

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(360)

<223>

<400> 27

cag gtc cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1

5

10

15

48

29/141

tca	gtg	aag	gtc	tcc	tgt	cag	gct	tct	gga	tac	atg	ttc	acc	ggc	ttc	96
Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe																
20							25						30			
tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg															144	
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met																
35							40						45			
gga tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt															192	
Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe																
50							55						60			
cag gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac															240	
Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr																
65							70						75		80	
atg gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt															288	
Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys																
85							90						95			
gct aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa															336	
Ala Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln																
100							105						110			
ggg aca atg gtc acc gtc tct tca															360	
Gly Thr Met Val Thr Val Ser Ser																
115							120									
<210> 28																
<211> 120																
<212> PRT																
<213> Homo sapiens																
<400> 28																

30 / 141

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe

20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35 40 45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe

50 55 60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr

65 70 75 80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Met Val Thr Val Ser Ser

115 120

<210> 29

<211> 348

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 29

31 / 141

cag gtc cag ctg gtg caa tct ggg gct gag gtg agg aag ccc ggg acg	48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Thr	
1 5 10 15	
aca gtg aca atc tcc tgc aag gtt tct gga cac aac ttc atc gac cac	96
Thr Val Thr Ile Ser Cys Lys Val Ser Gly His Asn Phe Ile Asp His	
20 25 30	
tac atg cat tgg gta caa cag gcc cct gga aaa ggg ctt gac tgg atg	144
Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Asp Trp Met	
35 40 45	
gga cta att gac cct gaa gat ggt cag acg aaa tat tca gag agg ttt	192
Gly Leu Ile Asp Pro Glu Asp Gly Gln Thr Lys Tyr Ser Glu Arg Phe	
50 55 60	
gag ggc aga gtc aca att acc gcg gac aag tca aca gac aca acc tac	240
Glu Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asp Thr Thr Tyr	
65 70 75 80	
ttg gag gtg agc ggc ctg aga tcg gaa gac acg gcc gtt tat ttc tgt	288
Leu Glu Val Ser Gly Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys	
85 90 95	
aca acg gac ttg ggt gac ttg aat tat tgg ggc cag gga acc ctg gtc	336
Thr Thr Asp Leu Gly Asp Leu Asn Tyr Trp Gly Gln Gly Thr Leu Val	
100 105 110	
acc gtc tcc tca	348
Thr Val Ser Ser	
115	

<210> 30

<211> 116

<212> PRT

3 2 / 1 4 1

<213> Homo sapiens

<400> 30

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Thr
1 5 10 15

Thr Val Thr Ile Ser Cys Lys Val Ser Gly His Asn Phe Ile Asp His
20 25 30

Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Asp Trp Met
35 40 45

Gly Leu Ile Asp Pro Glu Asp Gly Gln Thr Lys Tyr Ser Glu Arg Phe
50 55 60

Glu Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asp Thr Thr Tyr
65 70 75 80

Leu Glu Val Ser Gly Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Thr Thr Asp Leu Gly Asp Leu Asn Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 31

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(366)

33 / 141

<223>

<400> 31

cag gtc cag ctg gtg caa tct ggg gga ggc gtg gtc cag cct ggg agg 48
Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc aat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gca gtt ata tgg tat gat gga agt aat aaa tac tat gca gac tcc gtg 192
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac aca ctg tat 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg aga gat cac ggc ctt ggt gat caa gcc tcc tgg ttc gac ccc tgg 336
Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp
100 105 110

ggc cag ggc acc ctg gtc acc gtc tcc tca 366
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

3 4 / 1 4 1

<210> 32

<211> 122

<212> PRT

<213> Homo sapiens

<400> 32

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 33

<211> 368

<212> DNA

<213> Homo sapiens

35 / 141

<220>

<221> CDS

<222> (1)..(366)

<223>

<400> 33

cag gtc cag ctg gtg caa tct ggg gct gag gtg aag aag tct ggg gcc 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Ser Gly Ala
1 5 10 15

tca gtg aag gtc tcc tgc aag gct tct gga tac acc ttc acc ggc cac 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly His
20 25 30

ttt atc cac tgg gtg cgg cag gcc cct gga caa ggg ctt gag tgg atg 144
Phe Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

gga tgg atc aac cct aac gtt ggt gtc aca aat tat gca cag aag ttt 192
Gly Trp Ile Asn Pro Asn Val Gly Val Thr Asn Tyr Ala Gln Lys Phe
50 55 60

cag ggc agg gtc acc atg acc agg gac acg tcc ata agc aca gcc tac 240
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

ata gaa ctg agg agg ctg aga tct gac gac acg gcc gtg tat tac tgt 288
Ile Glu Leu Arg Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gtg aga gaa tcc gac aca gct gcg gtg gcc tac tac tac cac ggt atg 336
Val Arg Glu Ser Asp Thr Ala Ala Val Ala Tyr Tyr Tyr His Gly Met
100 105 110

gac gtc tgg gga caa tgg tca ccg tct ctt ca 368
Asp Val Trp Gly Gln Trp Ser Pro Ser Leu

36 / 141

115

120

<210> 34

<211> 122

<212> PRT

<213> Homo sapiens

<400> 34

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Ser Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly His

20 25 30

Phe Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35 40 45

Gly Trp Ile Asn Pro Asn Val Gly Val Thr Asn Tyr Ala Gln Lys Phe

50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr

65 70 75 80

Ile Glu Leu Arg Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Val Arg Glu Ser Asp Thr Ala Ala Val Ala Tyr Tyr Tyr His Gly Met

100 105 110

Asp Val Trp Gly Gln Trp Ser Pro Ser Leu

115 120

<210> 35

<211> 375

37 / 141

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(375)

<223>

<400> 35

cag gtc cag ctg gtg caa tct ggg gga gac tgg gta aag cct ggg ggg 48
Gln Val Gln Leu Val Gln Ser Gly Gly Asp Trp Val Lys Pro Gly Gly
1 5 10 15

tcc ctt aga ctc tcc tgt gca gcg tct gga ttc cct ttc gct aat gcc 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ala Asn Ala
20 25 30

tgg atg tat tgg ttc cgc cag gct cca ggg aag ggg ctg gag tgg gtt 144
Trp Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

ggc cgt att aaa agc aaa cca agt ggt ggg gct aca gag ttc gct gca 192
Gly Arg Ile Lys Ser Lys Pro Ser Gly Gly Ala Thr Glu Phe Ala Ala
50 55 60

ccc gtg gaa ggt aga ttc agc atc tcc aga gac gat tcg aaa aac acg 240
Pro Val Glu Gly Arg Phe Ser Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

atg gat ctg caa atg aat agc ctg aga acc gac gac aca gcc gta tat 288
Met Asp Leu Gln Met Asn Ser Leu Arg Thr Asp Asp Thr Ala Val Tyr
85 90 95

tat tgt acc aca gat tgg ggt tcg ggg acc tat cat aag ttt gct tta 336
Tyr Cys Thr Thr Asp Trp Gly Ser Gly Thr Tyr His Lys Phe Ala Leu
100 105 110

38 / 141

gat gtc tgg ggc caa ggg aca atg gtc acc gtc tct tca 375
Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120 125

<210> 36
<211> 125
<212> PRT
<213> Homo sapiens

<400> 36
Gln Val Gln Leu Val Gln Ser Gly Gly Asp Trp Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ala Asn Ala
20 25 30

Trp Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Arg Ile Lys Ser Lys Pro Ser Gly Gly Ala Thr Glu Phe Ala Ala
50 55 60

Pro Val Glu Gly Arg Phe Ser Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Met Asp Leu Gln Met Asn Ser Leu Arg Thr Asp Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Thr Asp Trp Gly Ser Gly Thr Tyr His Lys Phe Ala Leu
100 105 110

Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120 125

39 / 141

<210> 37

<211> 357

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 37

gtg cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc tca 48
Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
1 5 10 15

gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc tat 96
Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr
20 25 30

atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg gga 144
Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
35 40 45

tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt cag 192
Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln
50 55 60

gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac atg 240
Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met
65 70 75 80

gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt gcg 288
Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

40 / 141

aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa ggg 336
Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln Gly
100 105 110

aca atg gtc acc gtc tct tca 357
Thr Met Val Thr Val Ser Ser
115

<210> 38
<211> 119
<212> PRT
<213> Homo sapiens

<400> 38
Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
1 5 10 15

Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr
20 25 30

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
35 40 45

Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln
50 55 60

Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met
65 70 75 80

Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln Gly
100 105 110

4 1 / 1 4 1

Thr Met Val Thr Val Ser Ser

115

<210> 39

<211> 360

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(360)

<223>

<400> 39

cag gtg cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

tca gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc 96
Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe
20 25 30

tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

gga tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt 192
Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
50 55 60

cag gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac 240
Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
65 70 75 80

atg gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt 288

42 / 141

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa 336
Ala Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln
100 105 110

ggg aca atg gtc acc gtc tct tca 360
Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 40
<211> 120
<212> PRT
<213> Homo sapiens

<400> 40
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
50 55 60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
65 70 75 80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

43 / 141

Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 41
<211> 360
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(360)
<223>

<400> 41
cag gtc cag ctg gtg caa tct ggg gct gag gcg aag aag cct ggg gcc 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Ala Lys Lys Pro Gly Ala
1 5 10 15

tca gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc 96
Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe
20 25 30

tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

gga tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt 192
Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
50 55 60

cag gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac 240
Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr

44/141

65

70

75

80

atg gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt
Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys

288

85

90

95

gcg aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa
Ala Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln

336

100

105

110

ggg acc acg gtc acc gtc tcc tca
Gly Thr Thr Val Thr Val Ser Ser

360

115

120

<210> 42

<211> 120

<212> PRT

<213> Homo sapiens

<400> 42

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Ala Lys Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
50 55 60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
65 70 75 80

45 / 141

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 43

<211> 369

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(369)

<223>

<400> 43

cag gtc cag ctg gtg caa tct ggg gga ggc ttg gta cag cca ggg cgg 48
Gln Val Gln Leu Val Gln Ser Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

tcc ctg aga ctc tcc tgt aca act tct gga ttc acc ttt agt gat tat 96
Ser Leu Arg Leu Ser Cys Thr Thr Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

gct ttg agc tgg gtc cgc cag gct cca ggg agg ggg ctg gag tgg gta 144
Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
35 40 45

ggt ttc att aga aat aaa att tat ggt ggg aca aca gat tac gcc gca 192
Gly Phe Ile Arg Asn Lys Ile Tyr Gly Thr Thr Asp Tyr Ala Ala
50 55 60

46 / 141

tct	gtg	aaa	ggc	aga	ttc	acc	atc	tca	aga	gat	gat	tcc	aaa	agt	atc	240
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Ser	Ile	
65					70				75				80			
gcc	tat	ctg	caa	atg	aac	agc	ctg	aaa	acc	gag	gac	tca	gcc	gtc	tat	288
Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Thr	Glu	Asp	Ser	Ala	Val	Tyr	
					85				90				95			
tac	tgt	act	aga	gat	tcg	ggt	gtg	gtg	act	gct	gcc	tac	ttt	gac	tac	336
Tyr	Cys	Thr	Arg	Asp	Ser	Gly	Val	Val	Thr	Ala	Ala	Tyr	Phe	Asp	Tyr	
					100				105				110			
tgg	ggc	cag	ggc	acc	ctg	gtc	acc	gtc	tcc	tca						369
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser						
					115				120							
<210> 44																
<211> 123																
<212> PRT																
<213> Homo sapiens																
<400> 44																
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Arg	
1				5					10				15			
Ser	Leu	Arg	Leu	Ser	Cys	Thr	Thr	Ser	Gly	Phe	Thr	Phe	Ser	Asp	Tyr	
					20				25				30			
Ala	Leu	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Val	
					35				40				45			
Gly	Phe	Ile	Arg	Asn	Lys	Ile	Tyr	Gly	Gly	Thr	Thr	Asp	Tyr	Ala	Ala	
					50				55				60			

47 / 141

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65 70 75 80

Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Ser Ala Val Tyr
85 90 95

Tyr Cys Thr Arg Asp Ser Gly Val Val Thr Ala Ala Tyr Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 45

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(366)

<223>

<400> 45

cag gtc cag ctg gtg caa tct ggg gga ggc gtc cag cct ggg agg 48
Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc aat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

48/141

gca gtt ata tgg tat gat gga agt aat aaa tac tat gca gac tcc gtg	192	
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val		
50	55	60
aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac aca ctg tat	240	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr		
65	70	75
80		
ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt	288	
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys		
85	90	95
gcg aga gat cac ggc ctt ggt gat caa gcc tcc tgg ttc gac ccc tgg	336	
Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp		
100	105	110
ggc cag ggg acc acg gtc acc gtc tcc tca	366	
Gly Gln Gly Thr Thr Val Thr Val Ser Ser		
115	120	
<210> 46		
<211> 122		
<212> PRT		
<213> Homo sapiens		
<400> 46		
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg		
1	5	10
15		
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn		
20	25	30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val		
35	40	45

49 / 141

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 47

<211> 360

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(360)

<223>

<400> 47

cag gtc cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

tca gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc 96
Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe
20 25 30

tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144

50 / 141

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35 40 45

gga tgg atg aac act aac aat ggt gcc aca ggc tat gca cac aag ttt 192
Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
50 55 60

cag gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac 240
Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
65 70 75 80

atg gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt 288
Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa 336
Ala Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln
100 105 110

ggg aca atg gtc acc gtc tct tca 360
Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 48

<211> 120

<212> PRT

<213> Homo sapiens

<400> 48

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe
20 25 30

51 / 141

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
50 55 60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
65 70 75 80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 49

<211> 353

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(351)

<223>

<400> 49

cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc tca gtg 48
Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
1 5 10 15

aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc tat atg 96
Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr Met

5 2 / 1 4 1

20

25

30

cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg gga tgg 144
His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp

35

40

45

atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt cag gac 192
Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln Asp
50 55 60

agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac atg gag 240
Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met Glu
65 70 75 80

ctg ggc ggc ctg aca tct gac gac acg gcc gtc tat tat tgt gcg aga 288
Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
85 90 95

acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa ggg aca 336
Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln Gly Thr
100 105 110

atg gtc acc gtc tct tc 353
Met Val Thr Val Ser
115

<210> 50

<211> 117

<212> PRT

<213> Homo sapiens

<400> 50

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
1 5 10 15

53/141

Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr Met
20 25 30

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp
35 40 45

Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln Asp
50 55 60

Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met Glu
65 70 75 80

Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
85 90 95

Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln Gly Thr
100 105 110

Met Val Thr Val Ser
115

<210> 51
<211> 360
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(360)
<223>

<400> 51
cag gtc cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

54/141

tca gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc
 Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe
 20 25 30

tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

gga tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt
 Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
 50 55 60

cag gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac
 Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
 65 70 75 80

atg gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt
 Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa
 Ala Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln
 100 105 110

gga acc ctg gtc acc gtc tct tca
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 52
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 52

55 / 141

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe

20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35 40 45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe

50 55 60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr

65 70 75 80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 53

<211> 357

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 53

56 / 141

gtc cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc tca	48
Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser	
1 5 10 15	
gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc tat	96
Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr	
20 25 30	
atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg gga	144
Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly	
35 40 45	
tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt cag	192
Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln	
50 55 60	
gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac atg	240
Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met	
65 70 75 80	
gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt gcg	288
Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	
aga acc cag gag gtt tac tac tac gct atg gac gta ctg ggg cca agg	336
Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Leu Gly Pro Arg	
100 105 110	
gac aat ggt cac cgt ctc ttc	357
Asp Asn Gly His Arg Leu Phe	
115	

<210> 54

<211> 119

<212> PRT

5 7 / 1 4 1

<213> Homo sapiens

<400> 54

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
1 5 10 15

Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr
20 25 30

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
35 40 45

Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln
50 55 60

Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met
65 70 75 80

Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Thr Gln Glu Val Tyr Tyr Ala Met Asp Val Leu Gly Pro Arg
100 105 110

Asp Asn Gly His Arg Leu Phe
115

<210> 55

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(342)

58/141

<223>

<400> 55

gat att gtg atg acc cag act cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat agt act cct ccg acg ttc ggc caa ggg acc aag gtg gaa atc 336
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

aaa cgt 342
Lys Arg

59/141

<210> 56

<211> 114

<212> PRT

<213> Homo sapiens

<400> 56

Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser

20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln

35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val

50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

65 70 75 80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln

85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile

100 105 110

Lys Arg

<210> 57

<211> 337

<212> DNA

<213> Homo sapiens

6 0 / 1 4 1

<220>

<221> CDS

<222> (1)..(336)

<223>

<400> 57

gat ctt gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Leu Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tcc aac aat aag aac tac tta gct tgg cac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp His Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat agt act cct ccg acg ttc ggc caa ggg acc aaa gtg gat atc a 337
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Asp Ile
100 105 110

<210> 58

6 1 / 1 4 1

<211> 112

<212> PRT

<213> Homo sapiens

<400> 58

Asp Leu Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp His Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Asp Ile
100 105 110

<210> 59

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(342)

<223>

62 / 141

<400> 59

gat att gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat agt act cct ccg acg ttc ggc caa ggg acc aag gtg gaa atc 336
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

aaa cgt
Lys Arg 342

<210> 60

63/141

<211> 114

<212> PRT

<213> Homo sapiens

<400> 60

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg

<210> 61

<211> 342

<212> DNA

<213> Homo sapiens

<220>

64/141

<221> CDS

<222> (1)..(342)

<223>

<400> 61

gat att gtg atg act cag tct cca ctc tcc ctg ccc gtc acc cct gga 48
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ttg gat agt 96
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

gat gat gga aac acc tat ttg gac tgg tac ctg cag aag cca ggg cag 144
Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
35 40 45

tct cca cag ctc cta atc tat acg ctt tcc tat cgg gcc tct gga gtc 192
Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val
50 55 60

cca gac agg ttc agt ggc agt ggg tca ggc act gat ttc aca ctg aaa 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
65 70 75 80

atc agc agg gtg gag gct gag gat gtt gga gtt tat tac tgc atg caa 288
Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
85 90 95

cgt ata gag ttt cct tac act ttt ggc cag ggg acc aaa gtg gat atc 336
Arg Ile Glu Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Asp Ile
100 105 110

aaa cgt 342
Lys Arg

65 / 141

<210> 62

<211> 114

<212> PRT

<213> Homo sapiens

<400> 62

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
35 40 45

Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
65 70 75 80

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
85 90 95

Arg Ile Glu Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Asp Ile
100 105 110

Lys Arg

<210> 63

<211> 342

<212> DNA

66 / 141

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(342)

<223>

<400> 63

gat gtt gtg atg act cag tct cca ctc tcc ctg ccc gtc acc cct gga 48

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly

1 5 10 15

gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ttg gat agt 96

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser

20 25 30

gat gat gga aac acc tat ttg gac tgg tac ctg cag aag cca ggg cag 144

Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln

35 40 45

tct cca cag ctc cta atc tat acg ctt tcc tat cgg gcc tct gga gtc 192

Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val

50 55 60

cca gac agg ttc agt ggc agt ggg tca ggc act gat ttc aca ctg aaa 240

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys

65 70 75 80

atc agc agg gtg gag gct gag gat gtt gga gtt tat tac tgc atg caa 288

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln

85 90 95

cgt ata gag ttt cct tac act ttt ggc cag ggg acc aag gtg gaa atc 336

Arg Ile Glu Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile

100 105 110

67 / 141

aaa cgt

342

Lys Arg

<210> 64

<211> 114

<212> PRT

<213> Homo sapiens

<400> 64

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly

1

5

10

15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser

20

25

30

Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln

35

40

45

Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val

50

55

60

Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys

65

70

75

80

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln

85

90

95

Arg Ile Glu Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile

100

105

110

Lys Arg

68 / 141

<210> 65

<211> 339

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (339)

<223>

<400> 65

gat att gtg atg acc cag act cca ctc tcc ctg ccc gtc acc cct gga 48
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ttg gat agt 96
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

gat gat gga aac acc tat ttg gac tgg tac ctg cag aag cca ggg cag 144
Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
35 40 45

tct cca cag ctc cta atc tat acg ctt tcc tat cgg gcc tct gga gtc 192
Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val
50 55 60

cca gac agg ttc agt ggc agt ggg tca ggc act gat ttc aca ctg aaa 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
65 70 75 80

atc agc agg gtg gag gct gag gat gtt gga gtt tat tac tgc atg caa 288
Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
85 90 95

gct aca caa ttg tac act ttt ggc cag ggg acc aag gtg gag atc aaa 336

6 9 / 1 4 1

Ala Thr Gln Leu Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100

105

110

cgt

339

Arg

<210> 66

<211> 113

<212> PRT

<213> Homo sapiens

<400> 66

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly

1

5

10

15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser

20

25

30

Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln

35

40

45

Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val

50

55

60

Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys

65

70

75

80

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln

85

90

95

Ala Thr Gln Leu Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100

105

110

Arg

<210> 67
<211> 342
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (1)..(342)
<223>

<400> 67

gat att gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc	48		
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly			
1	5	10	15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

cct cct aaa ctg ctc att tac tgg gca tct acc cg_g gaa tcc ggg gtc 192
 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln

71 / 141

85

90

95

tat tat agt act cct ccg acg ttc ggc caa ggg acc aag ctg gag atc 336
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

aaa cgt 342
Lys Arg

<210> 68
<211> 114
<212> PRT
<213> Homo sapiens

<400> 68
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile

7 2 / 1 4 1

100

105

110

Lys Arg

<210> 69

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(342)

<223>

<400> 69

gat gtt gtg atg act cag act cca gac tcc ctg gct gtg tct ctg ggc 48

Asp Val Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly

1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta cac aag 96

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu His Lys

20 25 30

tcc aac aat aag aac tat tta gct tgg tac cag cag aaa cca gga cag 144

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln

35 40 45

cct cct aaa ttg ctc att cac tgg gct tct acc cgg gaa ttc ggg gtc 192

Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val

50 55 60

cct gac cga ctc agt ggc agc ggg tct gcg aca gat ttc act ctc acc 240

Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr

65 70 75 80

73 / 141

atc agc agc ctg cag gct gaa gac gtg gca gtc tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat gct gtt cct ctc acc ttc ggc caa ggg aca cga ctg gag att 336
Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
100 105 110

aaa cgt 342
Lys Arg

<210> 70
<211> 114
<212> PRT
<213> Homo sapiens

<400> 70
Asp Val Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu His Lys
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val
50 55 60

Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln

7 4 / 1 4 1

85

90

95

Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
100 105 110

Lys Arg

<210> 71

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(342)

<223>

<400> 71

gat att gtg atg acc cag acg cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

75 / 141

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat agt act cct ccg acg ttc agc caa ggg acc aag gtg gaa atc 336
Tyr Tyr Ser Thr Pro Pro Thr Phe Ser Gln Gly Thr Lys Val Glu Ile
100 105 110

aaa cgt 342
Lys Arg

<210> 72
<211> 114
<212> PRT
<213> Homo sapiens

<400> 72
Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

7 6 / 1 4 1

65 70 75 80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Ser Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg

<210> 73

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(342)

<223>

<400> 73

gat gtt gtg atg act cag tct cca gac tcc ctg act gtg tct ctg ggc 48
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Thr Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aag ctg ctc att tac tgg gca cct acc cgg gaa tcc ggg gtc 192

77 / 141

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Pro Thr Arg Glu Ser Gly Val
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat agt act cct ccg acg ttc ggc cag ggg acc aag gtg gaa atc 336
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

aaa cgt 342
Lys Arg

<210> 74
<211> 114
<212> PRT
<213> Homo sapiens

<400> 74
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Thr Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Pro Thr Arg Glu Ser Gly Val

78 / 141

50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg

<210> 75

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(342)

<223>

<400> 75

gat gtt gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag ggt gtt tta cac aag 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Gly Val Leu His Lys
20 25 30

tcc aac aat aag aac tat tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln

79 / 141

35

40

45

cct cct aaa ttg ctc att cac tgg gct tct acc cgg gaa ttc ggg gtc 192
Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val
50 55 60

cct gac cga ctc agt ggc agc ggg tct gcg aca gat ttc act ctc acc 240
Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc agc ctg cag gct gaa gac gtg gca gtc tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat gct gtt cct ctc acc ttc ggc caa ggg aca cga ctg gag att 336
Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
100 105 110

aaa cgt 342
Lys Arg

<210> 76
<211> 114
<212> PRT
<213> Homo sapiens

<400> 76
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Gly Val Leu His Lys
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln

80 / 141

35 40 45

Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val
50 55 60

Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
100 105 110

Lys Arg

<210> 77

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (342)

<223>

<400> 77

gat att gtg atg acc cag acg cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

81 / 141

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag	144	
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln		
35	40	45
cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc	192	
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val		
50	55	60
cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc	240	
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr		
65	70	75
80		
atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa	288	
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln		
85	90	95
tat tat agt act cct ccg acg ttc ggc caa ggg acc aag gtg gaa atc	336	
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile		
100	105	110
aaa cgt	342	
Lys Arg		

<210> 78
<211> 114
<212> PRT
<213> Homo sapiens

<400> 78
Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser

82/141

20

25

30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg

<210> 79

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(342)

<223>

<400> 79

gat gtt gtg atg act cag tct cca gac tcc ctg gct gtg cct ctg ggc
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Pro Leu Gly

1

5

10

15

48

83 / 141

gag	agg	gcc	acc	atc	aac	tgc	aag	tcc	agc	cag	agt	gtt	tta	cac	aag	96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu His Lys																
20								25						30		
tcc aac aat aag aac cat tta gct tgg tac cag cag aaa cca gga cag															144	
Ser Asn Asn Lys Asn His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln																
35								40						45		
cct cct aaa ttg ctc att cac tgg gct tct acc cgg gaa ttc ggg gtc															192	
Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val																
50								55						60		
cct gac cga ctc agt ggc agc ggg tct gcg aca gat ttc act ctc acc															240	
Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr																
65								70						75		80
atc aac agc ctg cag gct gaa gac gcg gca gtc tat tac tgt cag caa															288	
Ile Asn Ser Leu Gln Ala Glu Asp Ala Ala Val Tyr Tyr Cys Gln Gln																
85								90						95		
tat tat gct gtt cct ctc acc ttc ggc caa ggg aca cga ctg gag att															336	
Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile																
100								105						110		
aaa cgt															342	
Lys Arg																

<210> 80
<211> 114
<212> PRT
<213> Homo sapiens

<400> 80
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Pro Leu Gly

84/141

1

5

10

15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu His Lys
20 25 30

Ser Asn Asn Lys Asn His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val
50 55 60

Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Asn Ser Leu Gln Ala Glu Asp Ala Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
100 105 110

Lys Arg

<210> 81

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(342)

<223>

<400> 81

gat att gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc

48

85/141

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly

1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser

20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln

35 40 45

cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val

50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat agt act cct ccg acg ttc ggc caa ggg acc aaa gtg gat atc
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Asp Ile
100 105 110

aaa cgt
Lys Arg

<210> 82

<211> 114

<212> PRT

<213> Homo sapiens

86 / 141

<400> 82

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Asp Ile
100 105 110

Lys Arg

<210> 83

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(342)

<223>

87 / 141

<400> 83

gat gtt gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aaa ttg ctc att cac tgg gct tct acc cgg gaa ttc ggg gtc 192
Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val
50 55 60

cct gac cga ctc agt ggc agc ggg tct gcg aca gat ttc act ctc acc 240
Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc agc ctg cag gct gaa gac gtg gca gtc tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat gct gtt cct ctc acc ttc ggc caa ggg aca cga ctg gag att 336
Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
100 105 110

aaa cgt
Lys Arg 342

<210> 84

88/141

<211> 114

<212> PRT

<213> Homo sapiens

<400> 84

Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val
50 55 60

Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
100 105 110

Lys Arg

<210> 85

<211> 342

<212> DNA

<213> Homo sapiens

<220>

89 / 141

<221> CDS

<222> (1)..(342)

<223>

<400> 85

gac atc gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat agt act cct ccg acg ttc ggc caa ggg acc aag gtg gaa atc 336
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

aaa cgt 342
Lys Arg

90 / 141

<210> 86

<211> 114

<212> PRT

<213> Homo sapiens

<400> 86

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg

<210> 87

<211> 327

<212> DNA

91 / 141

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(327)

<223>

<400> 87

gaa att gtg ctg act cag tct cca ggc acc ctg tct ttg tct cca ggg 48
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

gaa aga gcc acc ctc tcc tgc aag gcc agt cag agt ttt agc agc aac 96
Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser Phe Ser Ser Asn
20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctg ctc 144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

ggc agt aaa tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
Gly Ser Lys Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

cct gaa gat ttt gca gtg tat tac tgt cag cag tat gtt acc tca ccg 288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Thr Ser Pro
85 90 95

tac act ttt ggc ctg ggg acc aag gtg gag atc aaa cgt 327
Tyr Thr Phe Gly Leu Gly Thr Lys Val Glu Ile Lys Arg
100 105

9 2 / 1 4 1

<210> 88

<211> 109

<212> PRT

<213> Homo sapiens

<400> 88

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser Phe Ser Ser Asn
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Thr Ser Pro
85 90 95

Tyr Thr Phe Gly Leu Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 89

<211> 325

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

93/141

<222> (1)..(324)

<223>

<400> 89

gat gtt ggg atg aca cag tct tca gcc acc cta tct ttg tct cca ggg 48
Asp Val Gly Met Thr Gln Ser Ser Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agg att agc agt tat 96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Ile Ser Ser Tyr
20 25 30

tta gcc tgg tac caa cag aaa cct ggc cag gct ccc aga ctc ctc atc 144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

tat gag gca gtc aaa agg gcc act ggc atc cca gcc agg ttc agt ggc 192
Tyr Glu Ala Val Lys Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

agt ggg tct ggg aca gag ttc acc ctc acc atc aac agc cta gag cct 240
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Glu Pro
65 70 75 80

gaa gat ttt gca gtt tat ttc tgt cag cag cgt ggc agc tgt cct ggg 288
Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Arg Gly Ser Cys Pro Gly
85 90 95

acg ttc ggc cag ggg acc aag ctg gag atc aaa cgt t 325
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 90

<211> 108

<212> PRT

94 / 141

<213> Homo sapiens

<400> 90

Asp Val Gly Met Thr Gln Ser Ser Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Ile Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Glu Ala Val Lys Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Arg Gly Ser Cys Pro Gly
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 91

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(366)

<223>

<400> 91

95/141

cag gtc cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc	48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala	
1 5 10 15	
tca gtg aag gtc tcc tgc aag gct tct gga tac acc ttc acc ggc tac	96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr	
20 25 30	
tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg	144
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	
35 40 45	
gga tgg atc aac cct aac agt ggt ggc aca aag tat gca cag aag ttt	192
Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala Gln Lys Phe	
50 55 60	
cag ggc agg gtc acc atg acc agg gac acg tcc atc agc aca gcc tac	240
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr	
65 70 75 80	
atg gag ctg agc agg ctg aga tct gac gac acg gcc gtg tat tac tgt	288
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gcg aga gga tac gat att ttg act ggt tat ggc tgg ttc gac ccc tgg	336
Ala Arg Gly Tyr Asp Ile Leu Thr Gly Tyr Gly Trp Phe Asp Pro Trp	
100 105 110	
ggc cag gga acc ctg gtc acc gtc tcc tca	366
Gly Gln Gly Thr Leu Val Thr Val Ser Ser	
115 120	

<210> 92

<211> 122

<212> PRT

96 / 141

<213> Homo sapiens

<400> 92

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Asp Ile Leu Thr Gly Tyr Gly Trp Phe Asp Pro Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 93

<211> 360

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(360)

97/141

<223>

<400> 93

cag gtc cag ctg gtg caa tct ggg gga ggc ttg gtc cag cct ggg ggg 48
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agt agc tat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

tgg atg agt tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtg 144
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gcc aac ata aag caa gat gga agt gag aaa tac tat gtg gac tct gtg 192
Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
50 55 60

aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac tca ctg tat 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

ctg caa atg aac acc ctg aga gcc gag gac acg gct gtg tat tac tgt 288
Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg aga gat cgt ttg tgg acc cag ggg ttt ttt gac tac tgg ggc cag 336
Ala Arg Asp Arg Leu Trp Thr Gln Gly Phe Phe Asp Tyr Trp Gly Gln
100 105 110

gga acc ctg gtc acc gtc tcc tca 360
Gly Thr Leu Val Thr Val Ser Ser
115 120

98/141

<210> 94

<211> 120

<212> PRT

<213> Homo sapiens

<400> 94

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Leu Trp Thr Gln Gly Phe Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 95

<211> 339

<212> DNA

<213> Homo sapiens

9 9 / 1 4 1

<220>

<221> CDS

<222> (1)..(339)

<223>

<400> 95

gac atc gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aac ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
Pro Pro Asn Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat act act ccg tgg acg ttc ggc caa ggg acc aag gtg gaa atc 336
Tyr Tyr Thr Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

aaa 339
Lys

100 / 141

<210> 96

<211> 113

<212> PRT

<213> Homo sapiens

<400> 96

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly

1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser

20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln

35 40 45

Pro Pro Asn Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val

50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln

85 90 95

Tyr Tyr Thr Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile

100 105 110

Lys

<210> 97

<211> 23

1 0 1 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 97

caggtkcagc tggtgcagtc tgg

23

<210> 98

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 98

caggtccagc ttgtgcagtc tgg

23

<210> 99

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 99

saggtccagc tggtacagtc tgg

23

<210> 100

<211> 23

1 0 2 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 100

caratcagc tggcagtc tgg

23

<210> 101

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 101

cagatcacct tgaaggagtc tggt

24

<210> 102

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 102

caggtcacct tgarggagtc tggt

24

<210> 103

<211> 23

1 0 3 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 103

gargtgcagc tggtggagtc tgg

23

<210> 104

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 104

caggtgcagc tggtggagtc tgg

23

<210> 105

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 105

gaggtgcagc tggtggagtc tgg

23

<210> 106

<211> 24

1 0 4 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 106

cagstgcagc tgcaggagtc gggc

24

<210> 107

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 107

caggtgcagc tacagcagtg gggc

24

<210> 108

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 108

gargtgcagc tggcagtc tgga

24

<210> 109

<211> 24

1 0 5 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 109

caggtacagc tgcagcagtc aggt

24

<210> 110

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 110

caggtscagc tggtgcaatc tgg

23

<210> 111

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 111

tgaggagacg gtgaccaggg tkcc

24

<210> 112

<211> 24

1 0 6 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 112

tgaagagacg gtgaccattg tccc

24

<210> 113

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 113

tgaggagacg gtgaccgtgg tccc

24

<210> 114

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 114

racatccaga tgacccagtc tcca

24

<210> 115

<211> 24

1 0 7 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 115

gmcatccagt tgacccagtc tcca

24

<210> 116

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 116

gccatccrga tgacccagtc tcca

24

<210> 117

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 117

gtcatctgga tgacccagtc tcca

24

<210> 118

<211> 24

1 0 8 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 118

gatatttgtga tgacccagac tcca

24

<210> 119

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 119

gatrttgtga tgactcagtc tcca

24

<210> 120

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 120

gaaatttgtgt tgacrcagtc tcca

24

<210> 121

<211> 24

1 0 9 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 121

gaaatagtga tgacgcagtc tcca

24

<210> 122

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 122

gaaatttgtaa tgacacagtc tcca

24

<210> 123

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 123

gacatcgtga tgacccagtc tcca

24

<210> 124

<211> 24

1 1 0 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 124

gaaacgacac tcacgcagtc tcca

24

<210> 125

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 125

gaaattgtgc tgactcagtc tcca

24

<210> 126

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 126

gatgttgtga tgacacagtc tcca

24

<210> 127

<211> 24

1 1 1 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 127

acgtttgatt tccaccttgg tccc

24

<210> 128

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 128

acgtttgatc tccascttgg tccc

24

<210> 129

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 129

acgtttgata tccactttgg tccc

24

<210> 130

<211> 24

1 1 2 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 130

acgtttaatc tccagtcgtg tccc

24

<210> 131

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 131

cagtctgtgc tgactcagcc accc

24

<210> 132

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 132

cagtctgtgy tgacgcagcc gccc

24

<210> 133

<211> 22

1 1 3 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 133

cagtctgccc tgactcagcc ts

22

<210> 134

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 134

tcctatgwgc tgactcagcc accc

24

<210> 135

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 135

tcctatgagc tgacacagcy accc

24

<210> 136

<211> 24

1 1 4 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 136

tcttctgagc tgactcagga ccct

24

<210> 137

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 137

tcctatgagc tgatgcagcc accc

24

<210> 138

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 138

cagcctgtgc tgactcaatc atcc

24

<210> 139

<211> 24

1 1 5 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 139

cagcttgtgc tgactcaatc gccc

24

<210> 140

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 140

ctgccttgtgc tgactcagcc cccg

24

<210> 141

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 141

cagccttgtgc tgactcagcc ayct

24

<210> 142

<211> 24

1 1 6 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 142

caggctgtgc tgactcagcc ggct

24

<210> 143

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 143

aattttatgc tgactcagcc ccac

24

<210> 144

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 144

cagrctgtgg tgactcagga gccc

24

<210> 145

<211> 24

1 1 7 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 145

cagactgtgg tgacccagga gcca

24

<210> 146

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 146

cwgccctgtgc tgactcagcc acct

24

<210> 147

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 147

caggcagggc tgactcagcc accc

24

<210> 148

<211> 24

1 1 8 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 148

accttaggacg gtgaccttgg tccc

24

<210> 149

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 149

accttaggacg gtcagcttgg tccc

24

<210> 150

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 150

accgaggacg gtcagctggg tgcc

24

<210> 151

<211> 91

1 1 9 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Template Linker Sequence

<400> 151

ggacaatggc caccgtctc tcaggtggc gtggttcggg tgggtggc tcgggtggc 60

gcggatcgga catccagatg acccagtctc c

91

<210> 152

<211> 28

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 152

gcaccctggc caccgtctcc tcaggtgg

28

<210> 153

<211> 28

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 153

ggacaatggc caccgtctc tcaggtgg

28

1 2 0 / 1 4 1

<210> 154

<211> 28

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 154

gaaccctggc caccgtctcc tcaggtgg

28

<210> 155

<211> 28

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 155

ggaccacggc caccgtctcc tcaggtgg

28

<210> 156

<211> 32

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 156

ggagactggc tcatctggat gtccgatccg cc

32

1 2 1 / 1 4 1

<210> 157

<211> 32

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 157

ggagactgag tcatcacaac atccgatccg cc

32

<210> 158

<211> 32

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 158

ggagactgcg tcaacacaat ttccgatccg cc

32

<210> 159

<211> 32

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 159

ggagactggg tcatcacgat gtccgatccg cc

32

1 2 2 / 1 4 1

<210> 160

<211> 32

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 160

ggagactgcg tgagtgtcgt ttccgatccg cc

32

<210> 161

<211> 32

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 161

ggagactgag tcagcacaat ttccgatccg cc

32

<210> 162

<211> 42

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 162

ggcggctgcg tcaacacaga ctgcgatccg ccaccgccag ag

42

1 2 3 / 1 4 1

<210> 163

<211> 42

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 163

gcaggctgag tcagagcaga ctgcgatccg ccaccgccag ag

42

<210> 164

<211> 42

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 164

ggtggctgag tcagcacata ggacgatccg ccaccgccag ag

42

<210> 165

<211> 42

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 165

gggtcctgag tcagctcaga agacgatccg ccaccgccag ag

42

1 2 4 / 1 4 1

<210> 166

<211> 42

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 166

ggcggttgag tcagtataac gtgcgatccg ccaccgccag ag

42

<210> 167

<211> 42

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 167

gacggctgag tcagcacaga ctgcgatccg ccaccgccag ag

42

<210> 168

<211> 42

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 168

tggggctgag tcagcataaa attcgatccg ccaccgccag ag

42

1 2 5 / 1 4 1

<210> 169

<211> 39

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 169

agtattgacc atggcccagg tgcagctggc gcagtctgg

39

<210> 170

<211> 39

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 170

agtattgacc atggcccagg tcaacttaag ggagtctgg

39

<210> 171

<211> 39

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 171

agtattgacc atggccgagg tgcagctggc ggagtctgg

39

1 2 6 / 1 4 1

<210> 172

<211> 39

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 172

agtattgacc atggcccagg tgcagctgca ggagtcggg

39

<210> 173

<211> 39

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 173

agtattgacc atggcccagg tgcagctgtt gcagtctgc

39

<210> 174

<211> 39

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 174

agtattgacc atggcccagg tacagctgca gcagtcagg

39

1 2 7 / 1 4 1

<210> 175

<211> 34

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 175

taatgaattc acgtttgatt tccaccttgg tccc

34

<210> 176

<211> 34

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 176

taatgaattc acgtttgatc tccagcttgg tccc

34

<210> 177

<211> 34

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 177

taatgaattc acgtttgata tccactttgg tccc

34

1 2 8 / 1 4 1

<210> 178

<211> 34

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 178

taatgaattc acgtttgatc tccacaccttgg tccc

34

<210> 179

<211> 34

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 179

taatgaattc acgtttaatc tccagtcgtg tccc

34

<210> 180

<211> 34

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 180

taatgaattc acctaggacg gtgacaccttgg tccc

34

1 2 9 / 1 4 1

<210> 181

<211> 34

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 181

taatgaattc acctaggacg gtcagcttgg tccc

34

<210> 182

<211> 34

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 182

taatgaattc acctaataacg gtgagctggg tccc

34

<210> 183

<211> 861

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(861)

<223>

<400> 183

atg aaa tac ctg ctg ccg acc gct gct gct ggt ctg ctg ctc ctc gct

48

130 / 141

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala

1

5

10

15

gcc cag ccg gcg atg gcc atg gcc cag gtg cag ctg gtg cag tct ggg
Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly

20

25

30

96

gct gag gtg aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gct
Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala

35

40

45

144

tct gga tac acc ttc acc ggc tac tat atg cac tgg gtg cga cag gcc
Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala

50

55

60

192

cct gga caa ggg ctt gag tgg atg gga tgg atc aac cct aac agt ggt
Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly
65 70 75 80

240

ggc aca aag tat gca cag aag ttt cag ggc agg gtc acc atg acc agg
Gly Thr Lys Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg
85 90 95

288

gac acg tcc atc agc aca gcc tac atg gag ctg agc agg ctg aga tct
Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser
100 105 110

336

gac gac acg gcc gtg tat tac tgt gcg aga gga tac gat att ttg act
Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Asp Ile Leu Thr
115 120 125

384

ggt tat ggc tgg ttc gac ccc tgg ggc cag gga acc ctg gtc acc gtc
Gly Tyr Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
130 135 140

432

tcc tca ggt ggt ggt ggt tcg ggt ggt ggt tcg ggt ggt ggc gga

480

1 3 1 / 1 4 1

Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly				
145	150	155	160	
tcg gac atc gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg				528
Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu				
165	170	175		
ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac				576
Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr				
180	185	190		
agc tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga				624
Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly				
195	200	205		
cag cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg				672
Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly				
210	215	220		
gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc				720
Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu				
225	230	235	240	
acc atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag				768
Thr Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln				
245	250	255		
caa tat tat agt act cct ccg acg ttc ggc caa ggg acc aag gtg gaa				816
Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu				
260	265	270		
atc aaa cgt cgt gaa ttc gac tac aag gat gac gac gat aag tga				861
Ile Lys Arg Arg Glu Phe Asp Tyr Lys Asp Asp Asp Lys				
275	280	285		

1 3 2 / 1 4 1

<210> 184

<211> 286

<212> PRT

<213> Homo sapiens

<400> 184

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly
20 25 30

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
35 40 45

Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala
50 55 60

Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly
65 70 75 80

Gly Thr Lys Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg
85 90 95

Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser
100 105 110

Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Asp Ile Leu Thr
115 120 125

Gly Tyr Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
130 135 140

Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

1 3 3 / 1 4 1

Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
165 170 175

Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr
180 185 190

Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
195 200 205

Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly
210 215 220

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
225 230 235 240

Thr Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
245 250 255

Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
260 265 270

Ile Lys Arg Arg Glu Phe Asp Tyr Lys Asp Asp Asp Lys
275 280 285

<210> 185

<211> 846

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(846)

<223>

<400> 185

1 3 4 / 1 4 1

atg	aaa	tac	ctg	ctg	ccg	acc	gct	gct	gct	ggt	ctg	ctg	ctc	ctc	gct	48	
Met	Lys	Tyr	Leu	Leu	Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu	Leu	Leu	Ala		
1		5			10						15						
gcc	cag	ccg	gcg	atg	gcc	atg	gcc	cag	gtg	cag	ctg	gtg	cag	tct	ggg	96	
Ala	Gln	Pro	Ala	Met	Ala	Met	Ala	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly		
				20				25					30				
gct	gag	gtg	aag	aag	cct	ggg	gcc	tca	gtg	aag	gtc	tcc	tgc	aag	gct	144	
Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala		
				35				40				45					
tct	gga	tac	acc	ttc	acc	ggc	tac	tat	atg	cac	tgg	gtg	cga	cag	gcc	192	
Ser	Gly	Tyr	Thr	Phe	Thr	Gly	Tyr	Tyr	Tyr	Met	His	Trp	Val	Arg	Gln	Ala	
				50				55				60					
cct	gga	caa	ggg	ctt	gag	tgg	atg	gga	tgg	atc	aac	cct	aac	agt	ggt	240	
Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Trp	Ile	Asn	Pro	Asn	Ser	Gly		
				65				70			75		80				
ggc	aca	aag	tat	gca	cag	aag	ttt	cag	ggc	agg	gtc	acc	atg	acc	agg	288	
Gly	Thr	Lys	Tyr	Ala	Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Met	Thr	Arg		
				85				90				95					
gac	acg	tcc	atc	agc	aca	gcc	tac	atg	gag	ctg	agc	agg	ctg	aga	tct	336	
Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser		
				100				105				110					
gac	gac	acg	gcc	gtg	tat	tac	tgt	gcg	aga	gga	tac	gat	att	ttg	act	384	
Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Tyr	Asp	Ile	Leu	Thr		
				115				120				125					
ggt	tat	ggc	tgg	ttc	gac	ccc	tgg	ggc	cag	gga	acc	ctg	gtc	acc	gtc	432	
Gly	Tyr	Gly	Trp	Phe	Asp	Pro	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val		
					130			135			140						

1 3 5 / 1 4 1

tcc tca ggt ggt ggt tcg ggt ggt ggt tcg ggt ggt ggc gga	480
Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly	
145 150 155 160	
tcg gaa att gtg ctg act cag tct cca ggc acc ctg tct ttg tct cca	528
Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro	
165 170 175	
ggg gaa aga gcc acc ctc tcc tgc aag gcc agt cag agt ttt agc agc	576
Gly Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser Phe Ser Ser	
180 185 190	
aac tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctg	624
Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu	
195 200 205	
ctc atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc	672
Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe	
210 215 220	
agt ggc agt aaa tct ggg aca gac ttc act ctc acc atc agc aga ctg	720
Ser Gly Ser Lys Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu	
225 230 235 240	
gag cct gaa gat ttt gca gtg tat tac tgt cag cag tat gtt acc tca	768
Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Thr Ser	
245 250 255	
ccg tac act ttt ggc cag ggg acc aag gtg gag atc aaa cgt cgt gaa	816
Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Arg Glu	
260 265 270	
ttc gac tac aag gat gac gac gat aag tga	846
Phe Asp Tyr Lys Asp Asp Asp Asp Lys	
275 280	

1 3 6 / 1 4 1

<210> 186

<211> 281

<212> PRT

<213> Homo sapiens

<400> 186

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly
20 25 30

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
35 40 45

Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala
50 55 60

Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly
65 70 75 80

Gly Thr Lys Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg
85 90 95

Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser
100 105 110

Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Asp Ile Leu Thr
115 120 125

Gly Tyr Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
130 135 140

Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

1 3 7 / 1 4 1

Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro
165 170 175

Gly Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser Phe Ser Ser
180 185 190

Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu
195 200 205

Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe
210 215 220

Ser Gly Ser Lys Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu
225 230 235 240

Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Thr Ser
245 250 255

Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Arg Glu
260 265 270

Phe Asp Tyr Lys Asp Asp Asp Asp Lys
275 280

<210> 187

<211> 852

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(852)

<223>

1 3 8 / 1 4 1

<400> 187

atg aaa tac ctg ctg ccg acc gct gct gct ggt ctg ctg ctc ctc gct 48
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15

gcc cag ccg gcg atg gcc atg gcc cag gtc cag ctg gtg caa tct ggg 96
 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly
 20 25 30

gga ggc ttg gtc cag cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc 144
 Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 35 40 45

tct gga ttc acc ttt agt agc tat tgg atg agt tgg gtc cgc cag gct 192
 Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val Arg Gln Ala
 50 55 60

cca ggg aag ggg ctg gag tgg gtg gcc aac ata aag caa gat gga agt 240
 Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile Lys Gln Asp Gly Ser
 65 70 75 80

gag aaa tac tat gtg gac tct gtg aag ggc cga ttc acc atc tcc aga 288
 Glu Lys Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
 85 90 95

gac aac gcc aag aac tca ctg tat ctg caa atg aac acc ctg aga gcc 336
 Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala
 100 105 110

gag gac acg gct gtg tat tac tgt gcg aga gat cgt ttg tgg acc cag 384
 Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Leu Trp Thr Gln
 115 120 125

ggg ttt ttt gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tca 432
 Gly Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 130 135 140

139 / 141

ggt ggt ggt ggt tcg ggt ggt ggt tcg ggt ggt ggc gga tcg gac	480		
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp			
145	150	155	160
atc gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc gag	528		
Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu			
165	170	175	
agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc tcc	576		
Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser			
180	185	190	
aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag cct	624		
Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro			
195	200	205	
cct aac ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc cct	672		
Pro Asn Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro			
210	215	220	
gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc atc	720		
Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile			
225	230	235	240
agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa tat	768		
Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr			
245	250	255	
tat act act ccg tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa	816		
Tyr Thr Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys			
260	265	270	
cgt gaa ttc gac tac aag gat gac gac gat aag tga	852		
Arg Glu Phe Asp Tyr Lys Asp Asp Asp Asp Lys			
275	280		

1 4 0 / 1 4 1

<210> 188

<211> 283

<212> PRT

<213> Homo sapiens

<400> 188

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly
20 25 30

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
35 40 45

Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val Arg Gln Ala
50 55 60

Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile Lys Gln Asp Gly Ser
65 70 75 80

Glu Lys Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
85 90 95

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala
100 105 110

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Leu Trp Thr Gln
115 120 125

Gly Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135 140

Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser Asp

1 4 1 / 1 4 1

145

150

155

160

Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu
165 170 175

Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser
180 185 190

Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro
195 200 205

Pro Asn Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro
210 215 220

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
225 230 235 240

Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr
245 250 255

Tyr Thr Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
260 265 270

Arg Glu Phe Asp Tyr Lys Asp Asp Asp Asp Lys

275

280